

D²

17. (Twice Amended) The polynucleotide of claim 9, wherein said polynucleotide codes for a protein which comprises an amino acid sequence having at least [70%] 90% identity [to] over the entire length of SEQUENCE ID NO. 17.

18. (Twice Amended) The polynucleotide of claim 9, wherein said polynucleotide comprises DNA having at least [70%] 90% identity [with] over the entire length of SEQUENCE ID NO. 14.

19. (Twice Amended) A recombinant expression system comprising a nucleic acid sequence that includes an open reading frame polynucleotide, wherein said open reading frame is operably linked to a control sequence compatible with a desired host and said nucleic acid sequence has at least [70%] 90% identity [with] over the entire length of an amino acid sequence selected from the group consisting of SEQUENCE ID NOS. 1-14, and complements thereof.

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24 (Twice Amended) A method for producing a polypeptide comprising at least one epitope, said method comprising incubating host cells that have been transfected with an expression vector containing a polynucleotide sequence encoding a polypeptide, wherein said polypeptide comprises an amino acid sequence compatible with a desired host, and said nucleic acid sequence has at least [70%] 90% identity [with] over the entire length of an amino acid sequence selected from the group consisting of SEQUENCE ID NOS. 17-21.

REMARKS

Claims 9, 13 – 20, and 24 are rejected by the Examiner under 35 U.S.C. §101 because the claimed invention lacks a credible, substantial, specific or a well-established utility. The Examiner states that the specification provides absolutely no evidence that the sequences of SEQ ID NO: 1 – 14 are correlated with any type of disease or condition of the breast.

Applicant disagrees due to the fact that these sequences are members of the RING finger family. Recently a new class of zinc-finger proteins was identified and designated as the RING finger family. The proteins in this family are characterized by the RING finger motif which is C-X₂-C-X₍₉₋₃₉₎-C-X₍₁₋₃₎-H-X₍₂₋₃₎-C-X₂-C-X₍₄₋₄₈₎-C-X₂-C, where X is